BLAST Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

Nucleotide Sequence (41 letters)

Results for: lcl|54211 None(41bp) ▾
Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
   lcl|54211
Description
   None
Molecule type
   nucleic acid
Query Length
   41

Subject ID
   54213
Description
   None
Molecule type
   nucleic acid
Subject Length
   78
Program
   BLASTN 2.2.21+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.
Other reports: Search Summary [Taxonomy reports]

Search Parameters

Program	blastn
Word size	7
Expect value	1000
Hitlist size	100
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.37406	1.37406

| K | 0 710603 | 0 710603 |
| H | 1 30725 | 1 30725 |

Results Statistics

Effective search space 2628

Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

Color key for alignment scores

| <40 | 40-50 | 50-80 | 80-200 | >=200 |

Query

| 0 | 8 | 16 | 24 | 32 | 40 |
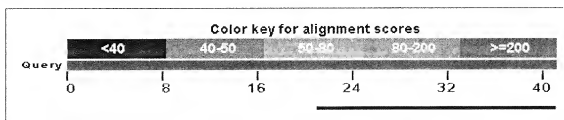
Dot Matrix View

Plot of lcl|54211 vs 54213 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

Descriptions

Legend for links to other resources: □ UniGene □ GEO □ Gene □ Structure □ Map Viewer

```
Sequences producing significant alignments:
(Click headers to sort columns)
54213                                          32.2  32.2  48%  5e-07 95%
```

Alignments Select All Get selected sequences Distance tree of results Multiple alignment NEW

```
>lcl|54213
Length=78

 Score = 32.2 bits (16),  Expect = 5e-07
 Identities = 19/20 (95%), Gaps = 0/20 (0%)
 Strand=Plus/Minus

Query  22  GCCCTCGCCCCTGGAGTTTG  41
           ||||| |||||||||||||||
Sbjct  78  GCCCTGGCCCCTGGAGTTTG  59
```

Select All Get selected sequences Distance tree of results Multiple alignment NEW